STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 148565

TO: Nita M Minnifield
Location: 3c01 / 3c18
Wednesday, March 23, 2005
Art Unit: 1646
Phone: 571-272-0860
Serial Number: 09 / 830839

From: Jan Delaval
Location: Biotech-Chem Library
Remsen 1a51
Phone: 571-272-22504

jan.delaval@uspto.gov

Search Notes

From:	Chan, Christina
Sent:	Tuesday, March 22, 2005 4:36 PM
To:	Minnifield, Nita; STIC-Biotech/ChemLib
Subject:	RE: interference search

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From:	Minnifield, Nita
Sent:	Tuesday, March 22, 2005 4:34 PM
To:	Chan, Christina
Subject:	interference search

Christina, please approve, 2 month amdt.

STIC

09/830839

Please do an interference sequence search on SEQ ID NO:1 and 6 of the above application.

Please provide a paper copy of the results.

Thanks,
Minnifield
71976
Art Unit 1645

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-250 4
Date Searcher Picked up: 3/23/05
Date Completed: 3/23/05
Searcher Prep/Rev. Time: 76
Online Time:_____

****
Type of Search

NA#:_____ AA#:__✓__
Interference:__✓__ SPDI:___
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:__✓___
WWW/Internet:_____
Other(Specify):_____

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: March 23, 2005, 06:57:56 ; Search time 93.5 Seconds
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Title: US-09-830-839-6
Perfect score: 77
Sequence: 1 WNFAGIEAAASAIQG 15

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Post-processing: Minimum Match 0%
                 Maximum Match 100%

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Listing first 45 summaries

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Published Applications AA:*
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SUMMARIES

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3	77	100.0	15	9	US-09-813-333-60 Sequence 60, Appl
4	77	100.0	20	13	US-10-044-703-60 Sequence 60, Appl
5	77	100.0	20	15	US-10-239-103-60 Sequence 60, Appl
6	77	100.0	15	20	US-09-886-349A-33 Sequence 33, Appl
7	77	100.0	15	11	US-10-193-002-99 Sequence 99, Appl
8	77	100.0	15	14	US-10-098-843-104 Sequence 104, Appl
9	77	100.0	51	14	US-10-084-732A-33 Sequence 33, Appl
10	77	100.0	51	11	US-09-805-427A-1 Sequence 1, Appl
11	77	100.0	95	9	US-09-872-505-1 Sequence 12, Appli
12	77	100.0	95	16	US-10-332-512A-12 Sequence 12, Appl
13	77	100.0	403	9	US-09-791-171-173 Sequence 173, App
14	77	100.0	403	9	US-09-805-427A-4 Sequence 4, Appli
15	77	100.0	403	10	US-09-804-980-173 Sequence 173, App
16	77	100.0	403	11	US-09-872-505-4 Sequence 4, Appli
17	77	100.0	403	16	US-10-620-246-173 Sequence 173, App
18	77	100.0	404	9	US-09-791-171-172 Sequence 172, App
19	77	100.0	404	9	US-09-805-804-172 Sequence 172, App
20	77	100.0	404	3	US-09-804-980-172 Sequence 172, App
21	77	100.0	404	11	US-09-872-505-3 Sequence 3, Appli
22	77	100.0	404	16	US-10-620-246-172 Sequence 172, App
23	66	85.7	20	9	US-09-813-333-61 Sequence 61, Appl
24	66	85.7	20	13	US-10-044-703-61 Sequence 61, Appl
25	66	85.7	20	15	US-10-239-103-61 Sequence 61, Appl
26	60	77.9	13	9	US-09-813-333-59 Sequence 59, Appl
27	60	77.9	13	13	US-10-239-103-59 Sequence 59, Appl
28	60	77.9	13	15	US-10-044-703-59 Sequence 59, Appl
29	54	70.1	15	14	US-10-079-167-79 Sequence 79, Appl
30	54	70.1	15	16	US-10-345-000-1 Sequence 1, Appli
31	43	55.8	16	15	US-09-767-701-40957 Sequence 40957, A
32	43	55.8	324	16	US-10-369-499-21850 Sequence 21850, A
33	42.5	55.2	400	15	US-10-369-647-560 Sequence 560, App
34	42	54.5	409	16	US-10-289-762-554 Sequence 554, App
35	42	54.5	1447	15	US-10-437-963-133273 Sequence 133273,
36	41	53.2	93	16	US-10-289-647-108079 Sequence 108079,
37	41	53.2	149	14	US-10-264-213-168 Sequence 168, App
38	41	53.2	282	15	US-10-282-930-113 Sequence 113, App
39	41	53.2	443	15	US-10-369-493-9058 Sequence 9058, Ap
40	41	53.2	445	14	US-10-282-1122A-76999 Sequence 76999, A
41	41	53.2	463	14	US-10-156-761-12653 Sequence 12653, A
42	41	53.2	528	15	US-10-282-1122A-50764 Sequence 50764, A
43	41	53.2	893	15	US-10-282-1122A-69721 Sequence 69721, A
44	40	51.9	419	16	US-10-437-963-168592 Sequence 168592,
45	40	51.9	934	16	US-10-437-963-164110 Sequence 164110,

ALIGNMENTS

RESULT 1
US-10-079-167-80
Sequence 80, Application US/10079167
Publication No. US20030138454A1
GENERAL INFORMATION:
  APPLICANT: Hill, Adrian V.S.
  APPLICANT: McShane, Helen
  APPLICANT: Gilbert, Sarah C.
  APPLICANT: Reece, William
  APPLICANT: Schneider, Joerg
  TITLE OF INVENTION: Vaccination Method
  FILE REFERENCE: 2907.1000-001
  CURRENT APPLICATION NUMBER: US/10/079,167
  CURRENT FILING DATE: 2002-02-19
  PRIOR APPLICATION NUMBER: US 09/454,204
  PRIOR FILING DATE: 2002-02-19
  PRIOR APPLICATION NUMBER: GB 00 23203.3
  PRIOR FILING DATE: 2001-09-21
  PRIOR APPLICATION NUMBER: PCT/GB01/04116
  PRIOR FILING DATE: 2001-09-13
  PRIOR APPLICATION NUMBER: US 09/454,204
  PRIOR FILING DATE: 1999-12-09
  PRIOR APPLICATION NUMBER: PCT/GB98/01681
  PRIOR FILING DATE: 1998-06-09
  PRIOR APPLICATION NUMBER: GB 97 11957.2
  PRIOR FILING DATE: 1997-06-09
  NUMBER OF SEQ ID NOS: 99
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 80
  LENGTH: 15
  TYPE: PRT
  ORGANISM: Unknown
  FEATURE:
  OTHER INFORMATION: T cell epitope in ESAT6
US-10-079-167-80

Query Match   100.0%; Score 77; DB 14; Length 15;
Best Local Similarity   100.0%; Pred. No. 2.5e-06;

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

Run on: March 23, 2005, 06:36:09 ; Search time 30.5 Seconds
(without alignments)
36.713 Million cell updates/sec

Title: US-09-830-839-1
Perfect score: 79
Sequence: 1 MTEQQWNFAGIEAAA 15
Scoring table: BLOSUM62
Sequence: Gapop 10.0 , Gapext 0.5
Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	79	100.0	51	4	US-09-072-596-99	Sequence 99, Appl
5	79	100.0	51	4	US-09-072-967-104	Sequence 104, App
6	79	100.0	95	2	US-09-465-640-2	Sequence 2, Appl
7	79	100.0	403	4	US-09-050-739-173	Sequence 173, App
8	79	100.0	404	4	US-09-050-739-172	Sequence 172, App
9	52	65.8	10	3	US-09-001-984C-77	Sequence 77, Appl
10	52	65.8	10	4	US-09-396-347F-77	Sequence 77, Appl
11	42	53.2	409	4	US-09-198-452A-554	Sequence 554, App
12	42	53.2	413	1	US-08-579-667-4	Sequence 4, Appl
13	42	53.2	413	1	US-08-438-185A-515	Sequence 515, App
14	42	53.2	578	4	US-09-949-016-9799	Sequence 9799, Ap
15	41	51.9	176	4	US-09-462-842-3	Sequence 3, Appl
16	41	51.9	176	4	US-09-393-171-3	Sequence 3, Appli
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18	39	49.4	538	4	US-09-252-991A-18026	Sequence 18026, A
19	39	49.4	928	4	US-09-252-991A-24200	Sequence 24200, A
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21	38	48.1	155	3	US-08-505-860C-3	Sequence 3, Appli
22	38	48.1	349	1	US-09-489-039A-13578	Sequence 13578, A
23	38	48.1	410	1	US-08-579-667-2	Sequence 2, Appli
24	38	48.1	410	1	US-08-579-667-8	Sequence 8, Appli
25	38	48.1	410	1	US-09-252-991A-3065	Sequence 3065, A
26	38	48.1	795	4	US-09-252-991A-30635	Sequence 30635, A
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28	38	48.1	2600	4	US-09-949-016-7309	Sequence 7309, Ap
29	37	46.8	331	4	US-09-489-039A-9639	Sequence 9639, Ap
30	37	46.8	435	4	US-09-252-991A-23220	Sequence 23220, A
31	37	46.8	493	4	US-09-540-236-2120	Sequence 2120, Ap
32	37	46.8	668	4	US-09-538-092-599	Sequence 599, App
33	36.5	46.2	820	4	US-09-134-000C-6437	Sequence 6437, App
34	36.5	46.2	934	1	US-08-215-805A-80	Sequence 80, Appl
35	36	45.6	88	4	US-09-270-767-33601	Sequence 33601, A
36	36	45.6	88	3	US-09-270-767-48818	Sequence 48818, A
37	36	45.6	149	4	US-09-634-238-265	Sequence 265, App
38	36	45.6	149	4	US-09-489-039A-8963	Sequence 8963, Ap
39	36	45.6	221	4	US-09-904-615-155	Sequence 155, App
40	36	45.6	282	4	US-09-724-623-113	Sequence 113, App
41	36	45.6	376	4	US-09-270-957-4	Sequence 4, Appli
42	36	45.6	376	4	US-09-270-957-19	Sequence 19, Appli
43	36	45.6	470	4	US-09-902-540-9896	Sequence 9896, Ap
44	36	45.6	602	3	US-09-149-727-2	Sequence 2, Appli
45	36	45.6	602	2	US-09-270-957-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-818-112-104
Sequence 104, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-104

Query Match 100.0%; Score 79; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

                                    GenCore version 5.1.6
                                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:            March 23, 2005, 06:57:56 ; Search time 93.5 Seconds
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                                             53.118 Million cell updates/sec

Title:
Perfect score:     79
Sequence:          1 MTEQWNFAGIEAAA 15

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters:   1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	79	100.0	15	14	US-10-079-167-79	Sequence 79, Appl
2	79	100.0	15	15	US-10-345-000-1	Sequence 1, Appl
3	79	100.0	51	15	US-09-886-349A-33	Sequence 33, Appl
4	79	100.0	51	14	US-10-193-002-99	Sequence 99, Appl
5	79	100.0	51	14	US-10-084-843-104	Sequence 104, Appl
6	79	100.0	51	14	US-10-098-732A-33	Sequence 33, Appl
7	79	100.0	95	11	US-09-805-427A-1	Sequence 1, Appli
8	79	100.0	95	11	US-09-872-505-1	Sequence 1, Appl
9	79	100.0	95	16	US-10-332-512A-12	Sequence 12, Appl
10	79	100.0	403	9	US-09-791-171-173	Sequence 173, Appl
11	79	100.0	403	9	US-09-805-427A-4	Sequence 4, App
12	79	100.0	403	10	US-09-804-980-173	Sequence 173, App
13	79	100.0	403	11	US-09-872-505-4	Sequence 4, Appli
14	79	100.0	403	16	US-10-620-246-173	Sequence 173, App
15	79	100.0	404	9	US-09-791-171-172	Sequence 172, Appli
16	79	100.0	404	9	US-09-805-427A-3	Sequence 3, Appli
17	79	100.0	404	10	US-09-804-980-172	Sequence 172, App
18	79	100.0	404	11	US-09-872-505-3	Sequence 3, Appl
19	79	100.0	404	16	US-10-620-246-172	Sequence 172, App
20	79	74.7	20	13	US-09-813-333-60	Sequence 60, Appl
21	79	74.7	20	15	US-10-044-703-60	Sequence 60, Appl
22	79	74.7	20	15	US-10-239-103-60	Sequence 60, Appl
23	79	68.4	15	14	US-10-282-122A-69721	Sequence 69721, A
24	79	68.4	15	15	US-09-813-333-59	Sequence 59, Appl
25	79	60.8	893	15	US-10-044-703-59	Sequence 59, Appl
26	79	54.4	15	15	US-10-239-103-59	Sequence 59, Appl
27	79	54.4	13	13	US-09-813-333-61	Sequence 61, Appl
28	79	54.4	13	13	US-10-044-703-61	Sequence 61, Appl
29	79	54.4	13	9	US-10-239-103-61	Sequence 61, Appl
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31	79	54.4	20	15	US-10-282-122A-16773	Sequence 16773, A
32	79	54.4	409	15	US-10-369-493-554	Sequence 554, App
33	79	54.4	911	15	US-10-282-122A-76999	Sequence 76999, A
34	79	53.2	176	14	US-09-738-626-4782	Sequence 4782, Ap
35	79	53.2	445	15	US-10-282-122A-68011	Sequence 68011, A
36	79	51.9	539	15	US-10-767-701-42935	Sequence 42935, A
37	79	51.9	295	9	US-10-289-762-554	Sequence 554, App
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39	79	50.6	243	14	US-10-369-493-8029	Sequence 8029, Appl
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42	79	49.4	176	16	US-10-425-114-62705	Sequence 62705, A
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44	79	49.4	916	15	US-10-282-122A-66644	Sequence 66644, A
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ALIGNMENTS

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RESULT 1
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; Sequence 79, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
;  APPLICANT: Hill, Adrian V.S.
;  APPLICANT: McShane, Helen
;  APPLICANT: Gilbert, Sarah C.
;  APPLICANT: Reece, William
;  APPLICANT: Schneider, Joerg
;  TITLE OF INVENTION: Vaccination Method
;  FILE REFERENCE: 2907.1000-001
;  CURRENT APPLICATION NUMBER: US/10/079,167
;  CURRENT FILING DATE: 2002-02-19
;  PRIOR APPLICATION NUMBER: PCT/GB01/04116
;  PRIOR FILING DATE: 2001-09-13
;  PRIOR APPLICATION NUMBER: US 09/454,204
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: PCT/GB98/01681
;  PRIOR FILING DATE: 1998-06-09
;  PRIOR APPLICATION NUMBER: GB 97 11957.2
;  PRIOR FILING DATE: 1997-06-09
;  PRIOR APPLICATION NUMBER: GB 00 23203.3
;  PRIOR FILING DATE: 2001-09-21
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn version 4.0
; SEQ ID NO 79
;  LENGTH: 15
;  TYPE: PRT
;  ORGANISM: Unknown
;  FEATURE:
;  OTHER INFORMATION: T cell epitope in ESAT6
US-10-079-167-79

Query Match             100.0%;  Score 79;  DB 14;  Length 15;
Best Local Similarity   100.0%;  Pred. No. 9.8e-07;
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: March. 23, 2005, 06:36:09 ; Search time 30.5 Seconds
                 (without alignments)
                 36.713 Million cell updates/sec

Title:
Perfect score: 77
Sequence: 1 WNFAGIEAAASAIQG 15

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	77	100.0	51	3	US-08-818-112-104	Sequence 104, App
2	77	100.0	51	3	US-08-818-111-99	Sequence 99, Appl
3	77	100.0	51	3	US-09-056-556-104	Sequence 104, App
4	77	100.0	51	3	US-09-072-596-99	Sequence 99, Appl
5	77	100.0	51	4	US-09-072-967-104	Sequence 104, App
6	77	100.0	95	2	US-08-465-640-2	Sequence 2, Appl
7	77	100.0	403	4	US-09-050-739-173	Sequence 173, App
8	77	100.0	404	4	US-09-050-739-172	Sequence 172, App
9	42.5	55.2	556	4	US-09-252-991A-17793	Sequence 17793, A
10	42	54.5	116	4	US-09-902-540-13488	Sequence 13488, A
11	42	54.5	409	4	US-09-198-452A-554	Sequence 554, App
12	42	54.5	413	4	US-09-438-185A-515	Sequence 515, App
13	41	53.2	149	4	US-09-634-238-265	Sequence 265, App
14	41	53.2	282	4	US-09-724-623-113	Sequence 113, Appl
15	40	51.9	2293	3	US-09-368-590-2	Sequence 2, Appl
16	40	51.9	2600	3	US-09-949-016-7309	Sequence 7309, Ap
17	39	50.6	221	4	US-09-904-615-155	Sequence 155, App
18	39	50.6	413	4	US-09-252-991A-29788	Sequence 29788, A
19	39	50.6	1138	4	US-09-489-039A-13574	Sequence 13574, A
20	38	49.4	185	4	US-09-489-039A-11336	Sequence 11336, A
21	38	49.4	349	4	US-09-489-039A-13578	Sequence 13578, A
22	38	49.4	365	4	US-09-489-039A-30166	Sequence 30166, A
23	38	49.4	418	3	US-09-252-893B-4	Sequence 4, Appli
24	38	49.4	435	4	US-09-202-893B-4	Sequence 23220, A
25	37	48.1	209	4	US-09-252-991A-23220	Sequence 24013, A
26	37	48.1	209	3	US-09-252-991A-24013	Sequence 9, Appli
27	37	48.1	472	4	US-09-902-540-15461	Sequence 15461, A
28	37	48.1	475	4	US-09-252-991A-20838	Sequence 20838, A
29	37	48.1	898	4	US-09-902-540-11561	Sequence 11561, A
30	37	48.1	947	4	US-09-252-991A-21335	Sequence 21335, A
31	37	48.1	981	4	US-09-902-540-9848	Sequence 9848, Ap
32	37	48.1	1138	4	US-09-252-991A-25952	Sequence 25952, A
33	37	48.1	1223	4	US-09-538-092-777	Sequence 777, App
34	36	46.8	294	4	US-09-489-039A-10933	Sequence 10933, A
35	36	46.8	323	4	US-09-489-039A-13907	Sequence 13907, A
36	36	46.8	323	4	US-09-489-039A-10986	Sequence 10986, A
37	36	46.8	368	4	US-09-489-039A-13753	Sequence 13753, A
38	36	46.8	389	4	US-09-489-039A-8540	Sequence 8540, Ap
39	36	46.8	429	4	US-09-134-000C-3817	Sequence 3817, Ap
40	36	46.8	483	4	US-09-489-033A-13018	Sequence 13018, A
41	36	46.8	578	4	US-09-949-016-9799	Sequence 9799, Ap
42	36	46.8	630	4	US-09-248-796A-25512	Sequence 25512, A
43	36	46.8	759	4	US-09-902-540-16161	Sequence 16161, A
44	36	46.8	1534	4	US-09-543-611A-5182	Sequence 5182, Ap
45	35.5	46.1	467	4	US-09-252-991A-29729	Sequence 29729, A

ALIGNMENTS

RESULT 1
US-08-818-112-104
Sequence 104, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Dillon, Davin C.
;   APPLICANT: Campos-Neto, Antonio
;   APPLICANT: Houghton, Raymond
;   APPLICANT: Vedvick, Thomas S.
;   APPLICANT: Twardzik, Daniel R.
;   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
;   NUMBER OF SEQUENCES: 153
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SEED and BERRY LLP
;   STREET: 6300 Columbia Center, 701 Fifth Avenue
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98104-7092
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/818,112
;   FILING DATE: 13-MAR-1997
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Maki, David J.
;   REGISTRATION NUMBER: 31,392
;   REFERENCE/DOCKET NUMBER: 210121.411C6
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 622-4900
;   TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 104:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 51 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-818-112-104

Query Match   100.0%; Score 77; DB 3; Length 51;
Best Local Similarity   100.0%; Pred. No. 1.6e-06;
Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;